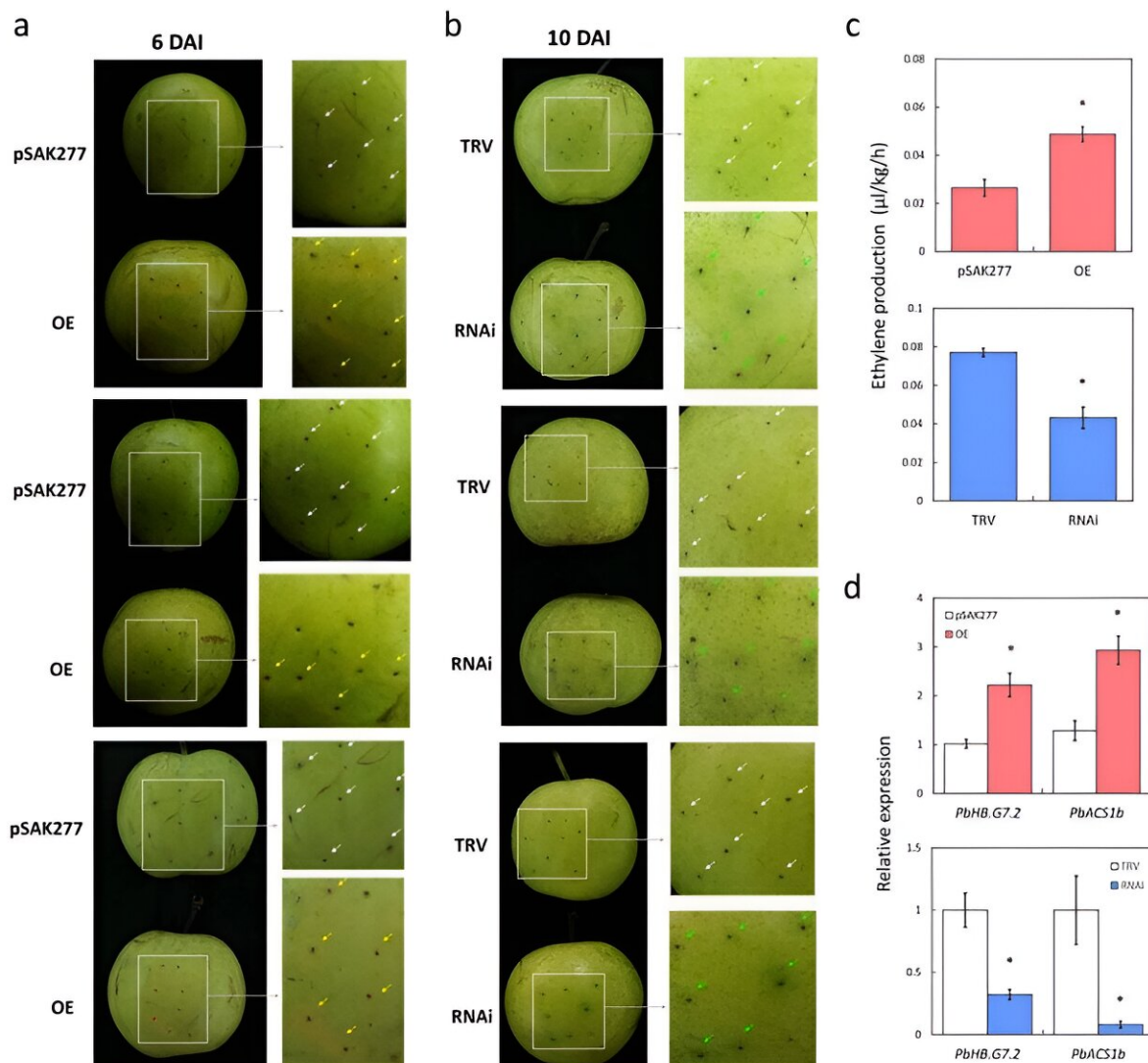


Ripe for discovery: Unraveling the genetic switches of pear maturation

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Regulation of PbHB.G7.2 on fruit ripening and ethylene biosynthesis. Credit: *Horticulture Research* (2024). DOI: 10.1093/hr/uhae086

Fruit ripening involves complex metabolic changes that affect sensory traits like color, flavor, and texture, making fruits more appealing for consumption. These changes are particularly pronounced in climacteric fruits, which experience a surge in ethylene production.

Ethylene biosynthesis is regulated by various [transcription factors](#), but the specifics of this regulation in pears remain largely unknown. Based on these challenges, it is essential to conduct in-depth research on the genetic and [molecular mechanisms](#) driving pear fruit ripening.

Researchers from Nanjing Agricultural University, have identified a key homeodomain transcription factor involved in pear fruit ripening. Their [study](#), published on March 28, 2024, in the journal *Horticulture Research*, explores how PbHB.G7.2 regulates ethylene biosynthesis by binding to the PbACS1b gene promoter.

This research uncovers new insights into the genetic control of fruit ripening, paving the way for advancements in horticultural practices.

The study focused on identifying transcription factors involved in ethylene biosynthesis during pear fruit ripening. Through transcriptome analysis, the researchers identified PbHB.G7.2, which directly binds to the promoter of PbACS1b, enhancing its activity and increasing ethylene production.

PbHB.G7.2 interacts with other homeodomain transcription factors, PbHB.G1 and PbHB.G2.1, disrupting its transcriptional activation. These interactions are crucial as they regulate the levels of ethylene produced, affecting the ripening process.

In over-expression experiments, PbHB.G7.2 significantly increased

ethylene production in pear fruit callus, confirming its role in ethylene biosynthesis. The dual-luciferase assay demonstrated that PbHB.G7.2 enhances the PbACS1b promoter's activity, pinpointing the binding region within the upstream sequence of the gene.

The researchers further validated the physical interaction between PbHB.G7.2 and the PbACS1b promoter through electrophoretic mobility shift assays.

Dr. Shao-Ling Zhang, a senior researcher at Nanjing Agricultural University, stated, "This discovery is a significant advancement in our understanding of the genetic regulation of fruit ripening. Identifying PbHB.G7.2 as a key regulator of ethylene biosynthesis provides valuable insights that can be applied to improve pear cultivation and enhance fruit quality. This research highlights the importance of molecular studies in addressing agricultural challenges."

The identification of PbHB.G7.2's role in [ethylene](#) biosynthesis during [pear](#) fruit ripening opens new avenues for developing targeted breeding strategies to improve fruit quality. By manipulating the expression of this transcription factor, it may be possible to control the ripening process, leading to longer shelf life and better-tasting fruit.

Additionally, these findings could be applied to other climacteric fruits, offering broader implications for horticulture and agriculture industries. This research underscores the potential of genetic studies in advancing agricultural practices and ensuring food security.

More information: Su-Hao Cao et al, Interaction among homeodomain transcription factors mediates ethylene biosynthesis during pear fruit ripening, *Horticulture Research* (2024). [DOI: 10.1093/hr/uhae086](https://doi.org/10.1093/hr/uhae086)

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